

Substitute Sequence Listing

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Substitute Sequence Listing																
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gac Asp 45	ttt Phe	att Ile	tat Tyr	caa Gln	gat Asp 50	ggc Gly	ttt Phe	agt Ser	act Thr	gca Ala 55	ggg Gly	att Ile	aca Thr	caa Gln	att Ile 60	195
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cat His 125	gga Gly	tat Tyr	gct Ala	ctt Leu	cag Gln 130	ggt Gly	tgg Trp	aaa Lys	att Ile	gat Asp 135	aat Asn	act Thr	gaa Glu	ggg Gly	cca Pro 140	435
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Substitute Sequence Listing															
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Pro	Ala	Glu	Val	Ser	Asn	Asn	Gly	Phe	Pro	Met	Ile	Val	Ala	Asn	Phe
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Substitute Sequence Listing

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 <213> Lawsonia intracellularis

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Substitute Sequence Listing

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Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly
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Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln
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Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly
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Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser Leu Phe Asn Ile
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Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro Pro Met Pro Glu
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Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val Gly Gly Asn Ile
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Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu Met Ser Gly Thr
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Substitute Sequence Listing

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Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr Pro Ala Glu Val
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Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr Thr Phe Phe Thr
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Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp Asn Thr Trp Lys
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Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys Lys Thr His Asn
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Substitute Sequence Listing

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Phe Thr Val Gly Ile Ile Met Leu Ile Leu Ala Cys Leu Ala Ala Leu
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Substitute Sequence Listing																
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aca Thr	tta Leu	ctc Leu	tca Ser 75	agt Ser	agt Ser	aat Asn	aga Arg	aat Asn 80	aca Thr	ata Ile	caa Gln	gcc Ala	ggt Gly 85	act Thr	cca Pro	292
cat His	caa Gln	gaa Glu 90	aat Asn	aac Asn	ata Ile	aaa Lys	gaa Glu 95	gat Asp	ctt Leu	caa Gln	ctg Leu	act Thr 100	aac Asn	aaa Lys	aat Asn	340
gaa Glu	caa Gln 105	aca Thr	act Thr	cca Pro	gaa Glu	gaa Glu 110	gaa Glu	gaa Glu	agt Ser	aaa Lys 115	ttt Phe	att Ile	tgg Trp	tta Leu		388
aca Thr 120	gaa Glu	gct Ala	cca Pro	tca Ser	gag Glu 125	ctt Leu	aaa Lys	aaa Lys	gga Gly	gaa Glu 130	aaa Lys	gct Ala	ata Ile	aca Thr	caa Gln 135	436
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cct Pro 185	aca Thr	aat Asn	cct Pro	tgg Trp	tta Leu	aaa Lys 190	aaa Lys	ata Ile	cgc Arg	tta Leu	ggt Gly 195	act Thr	aat Asn	aat Asn	gga Gly	628
aat Asn 200	aca Thr	cga Arg	ctt Leu	gtc Val	ttt Phe 205	gat Asp	ctt Leu	caa Gln	aaa Lys	aaa Lys 210	cca Pro	tct Ser	aaa Lys	act Thr	gaa Glu 215	676
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Substitute Sequence Listing

Tyr Gln Glu Asp Gly Gln Met Val Thr Gly Ile Ile Ser Lys Ile Ile
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Gly Ser Asn Cys Asp Asn Ser Ser Thr Ser Asp Ile Asn Asn Lys Lys
50 55 60

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Thr Ile Gln Ala Gly Thr Pro His Gln Glu Asn Asn Ile Lys Glu Asp
85 90 95

Leu Gln Leu Thr Asn Lys Asn Glu Gln Thr Thr Pro Glu Glu Glu Glu
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115 120 125

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130 135 140

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145 150 155 160

Leu Lys Asn Pro Asp Arg Phe Val Leu Asp Leu Gln Gly Lys Trp Gly
165 170 175

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180 185 190

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10 15 20

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Asn Ala Ala Ser Tyr Val Val Leu Pro Phe Lys Val Asn Ala Pro Pro
25 30 35

agc tat act tat ttg gaa aaa gct atc cca tct atg tta act tct aga 198
 Ser Tyr Thr Tyr Leu Glu Lys Ala Ile Pro Ser Met Leu Thr Ser Arg
 40 45 50 55

ctt tat tgg gaa gaa cgt ttt caa cct atc ccg gat gct aat gct att 246
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60 65 70

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Lys Ala Gly Lys Val Glu Asp Ile Lys Glu Met Asp Lys Ala Arg Ile
75 80 85

gct aca ggt gca gac tat ctt ata tgg gga cag gta aat att gta ggt 342
Ala Thr Gly Ala Asp Tyr Leu Ile Trp Gly Gln Val Asn Ile Val Gly
90 95 100

gat gaa gct acg ctt gat gta caa gtt tgt gat ata gaa gga tca att 390
Asp Glu Ala Thr Leu Asp Val Gln Val Cys Asp Ile Glu Gly Ser Ile
105 110 115

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 Trp Arg Lys Ser Lys Asn Thr Lys Val Asp Asn Leu Ile Thr Ala Leu
 120 125 130 135

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Gln Asp Thr Ala Asp Ala Ile Asn Ser Glu Leu Phe Gly Arg Ala Thr
140 145 150

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155 160 165

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Leu Ile Lys Gly Lys Gly Asn Glu Asn Gln Ser Tyr Leu Asn Pro Glu
170 175 180

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Phe Arg Tyr Gln Gly Ser Asn Leu Ser Arg Gly Arg Ser Gln Ala Leu
185 190 195

CCC ttt gct tca gtt ggt ata gtt gtt ggt gac ttt ata gga gat aat 678
Pro Phe Ala Ser Val Gly Ile Val Val Gly Asp Phe Ile Gly Asp Asn
200 205 210 215

aaa aat gaa gtt gcc ata tta agt gag tat aaa gtc cat att tat cga 726
Lys Asn Glu Val Ala Ile Leu Ser Glu Tyr Lys Val His Ile Tyr Arg
220 225 230

tgg gaa gaa gaa agg tta gct ctt ctt gga gaa tat aaa ttc cct cgc 774

Substitute Sequence Listing																
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Val	Gln	Glu	Ile	Ile	Val	Ser	Cys	Phe	Asp	Pro	Ser	Tyr	Ala	Lys	Pro	
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280					285					290					295	
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Thr	Asn	Leu	Pro	Phe	Tyr	Leu	Asn	Val	Val	Lys	Leu	Pro	Pro	Asp	Phe	
				300				305						310		
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Ser	Pro	Met	Leu	Ile	Gly	Gln	Lys	Ser	Asp	Asn	Ser	Arg	Ile	Phe	Ser	
			315					320					325			
ccc	tct	ggg	gtt	tat	gaa	ata	gaa	aaa	cat	gga	cgt	aac	tat	ata	atg	1062
Pro	Ser	Gly	Val	Tyr	Glu	Ile	Glu	Lys	His	Gly	Arg	Asn	Tyr	Ile	Met	
		330					335					340				
gga	aat	cgt	ctt	agt	ctt	cca	aag	gaa	gct	aat	att	ttt	aat	ttt	tct	1110
Gly	Asn	Arg	Leu	Ser	Leu	Pro	Lys	Glu	Ala	Asn	Ile	Phe	Asn	Phe	Ser	
	345					350					355					
tgg	tta	cca	tca	gat	tca	tta	aaa	gat	gaa	gaa	gct	aag	tta	gta	ctt	1158
Trp	Leu	Pro	Ser	Asp	Ser	Leu	Lys	Asp	Glu	Glu	Ala	Lys	Leu	Val	Leu	
360					365				370					375		
gta	acc	aat	aat	gaa	aga	tta	gtt	gta	tat	aat	aca	aaa	ggt	aca	aga	1206
Val	Thr	Asn	Asn	Glu	Arg	Leu	Val	Val	Tyr	Asn	Thr	Lys	Gly	Thr	Arg	
				380				385						390		
ctt	ttt	atg	act	gaa	gaa	gtg	tat	tat	ggt	tct	tct	gtt	ggt	ata	gac	1254
Leu	Phe	Met	Thr	Glu	Glu	Val	Tyr	Tyr	Gly	Ser	Ser	Val	Gly	Ile	Asp	
			395				400						405			
gag	ccc	agt	aat	atg	cct	ggt	ctt	gga	aag	tca	aaa	gag	ctt	atc	cct	1302
Glu	Pro	Ser	Asn	Met	Pro	Gly	Leu	Gly	Lys	Ser	Lys	Glu	Leu	Ile	Pro	
		410				415						420				
tct	aaa	tat	ttt	atc	cca	gga	cgg	atg	att	cct	att	aat	ctt	gat	tca	1350
Ser	Lys	Tyr	Phe	Ile	Pro	Gly	Arg	Met	Ile	Pro	Ile	Asn	Leu	Asp	Ser	
	425					430					435					
atg	ggg	aaa	tgg	gag	ttg	ctt	gta	agc	aag	cca	att	tct	gtt	gca	gca	1398
Met	Gly	Lys	Trp	Glu	Leu	Leu	Val	Ser	Lys	Pro	Ile	Ser	Val	Ala	Ala	
440				445						450				455		
aaa	ttt	ttt	gaa	aat	tat	aga	tct	ttt	gct	gaa	ggc	gaa	att	cag	gct	1446
Lys	Phe	Phe	Glu	Asn	Tyr	Arg	Ser	Phe	Ala	Glu	Gly	Glu	Ile	Gln	Ala	
			460					465						470		
tta	aca	tgg	gac	ggc	tta	gga	tta	ggt	ctt	gta	tgg	aat	aca	cgt	cgt	1494
Leu	Thr	Trp	Asp	Gly	Leu	Gly	Leu	Gly	Leu	Val	Trp	Asn	Thr	Arg	Arg	
			475					480					485			

Substitute Sequence Listing

att aag gga act att aca gat ttt gcc tta gct gat atg aat aat gat	1542
Ile Lys Gly Thr Ile Thr Asp Phe Ala Leu Ala Asp Met Asn Asn Asp	
490 495 500	
ggg aag tta gac tta gtt gtt tcc gtt aat agc cat aca ggg att ctt	1590
Gly Lys Leu Asp Leu Val Val Ser Val Asn Ser His Thr Gly Ile Leu	
505 510 515	
gga cta gaa aaa cga aag aca att ata gta ttt tat cct tta gag gta	1638
Gly Leu Glu Lys Arg Lys Thr Ile Ile Val Phe Tyr Pro Leu Glu Val	
520 525 530 535	
gat aaa caa ggt atc cct aag gct gtt gaa gat aac taa ttttttccta	1687
Asp Lys Gln Gly Ile Pro Lys Ala Val Glu Asp Asn	
540 545	
ttaattatatt ttttattctg atagttaa	1715

<210> 6
 <211> 547
 <212> PRT
 <213> Lawsonia intracellularis
 <400> 6

Met His Gln Lys Ser Cys Leu Val Ala Leu Cys Ile Met Phe Ile Ile
1 5 10 15
Met Val Gln Val Leu Gln Ala Asn Ala Ala Ser Tyr Val Val Leu Pro
20 25 30
Phe Lys Val Asn Ala Pro Pro Ser Tyr Thr Tyr Leu Glu Lys Ala Ile
35 40 45
Pro Ser Met Leu Thr Ser Arg Leu Tyr Trp Glu Glu Arg Phe Gln Pro
50 55 60
Ile Pro Asp Ala Asn Ala Ile Lys Ala Gly Lys Val Glu Asp Ile Lys
65 70 75 80
Glu Met Asp Lys Ala Arg Ile Ala Thr Gly Ala Asp Tyr Leu Ile Trp
85 90 95
Gly Gln Val Asn Ile Val Gly Asp Glu Ala Thr Leu Asp Val Gln Val
100 105 110
Cys Asp Ile Glu Gly Ser Ile Trp Arg Lys Ser Lys Asn Thr Lys Val
115 120 125
Asp Asn Leu Ile Thr Ala Leu Gln Asp Thr Ala Asp Ala Ile Asn Ser
130 135 140
Glu Leu Phe Gly Arg Ala Thr Thr Lys Pro Ser Ser Lys Ala Thr Ile

Substitute Sequence Listing															
145											150	155	160		
Val	Ala	Gln	Met	Asn 165	Ser	Gly	Leu	Ile	Lys 170	Gly	Lys	Gly	Asn	Glu 175	Asn
Gln	Ser	Tyr	Leu 180	Asn	Pro	Glu	Phe	Arg 185	Tyr	Gln	Gly	Ser	Asn 190	Leu	Ser
Arg	Gly	Arg 195	Ser	Gln	Ala	Leu	Pro 200	Phe	Ala	Ser	Val	Gly 205	Ile	Val	Val
Gly	Asp 210	Phe	Ile	Gly	Asp	Asn 215	Lys	Asn	Glu	Val	Ala 220	Ile	Leu	Ser	Glu
Tyr 225	Lys	Val	His	Ile	Tyr 230	Arg	Trp	Glu	Glu	Glu 235	Arg	Leu	Ala	Leu	Leu 240
Gly	Glu	Tyr	Lys	Phe 245	Pro	Arg	Ser	Leu	Gln 250	Ser	Leu	His	Ile	Arg 255	Ala
Phe	Asp	Val	Asp 260	His	Asp	Gly	Val	Gln 265	Glu	Ile	Ile	Val	Ser 270	Cys	Phe
Asp	Pro	Ser 275	Tyr	Ala	Lys	Pro	Tyr 280	Ser	Phe	Ile	Leu	Ser 285	Phe	Lys	Asn
Arg	Val 290	Phe	Lys	Glu	Leu	Ala 295	Thr	Asn	Leu	Pro	Phe 300	Tyr	Leu	Asn	Val
Val 305	Lys	Leu	Pro	Pro	Asp 310	Phe	Ser	Pro	Met	Leu 315	Ile	Gly	Gln	Lys	Ser 320
Asp	Asn	Ser	Arg	Ile 325	Phe	Ser	Pro	Ser	Gly 330	Val	Tyr	Glu	Ile	Glu 335	Lys
His	Gly	Arg	Asn 340	Tyr	Ile	Met	Gly	Asn 345	Arg	Leu	Ser	Leu	Pro 350	Lys	Glu
Ala	Asn	Ile 355	Phe	Asn	Phe	Ser	Trp 360	Leu	Pro	Ser	Asp	Ser 365	Leu	Lys	Asp
Glu	Glu 370	Ala	Lys	Leu	Val	Leu 375	Val	Thr	Asn	Asn	Glu 380	Arg	Leu	Val	Val
Tyr 385	Asn	Thr	Lys	Gly	Thr 390	Arg	Leu	Phe	Met	Thr 395	Glu	Glu	Val	Tyr	Tyr 400

Substitute Sequence Listing

Gly Ser Ser Val Gly Ile Asp Glu Pro Ser Asn Met Pro Gly Leu Gly
405 410 415

Lys Ser Lys Glu Leu Ile Pro Ser Lys Tyr Phe Ile Pro Gly Arg Met
420 425 430

Ile Pro Ile Asn Leu Asp Ser Met Gly Lys Trp Glu Leu Leu Val Ser
435 440 445

Lys Pro Ile Ser Val Ala Ala Lys Phe Phe Glu Asn Tyr Arg Ser Phe
450 455 460

Ala Glu Gly Glu Ile Gln Ala Leu Thr Trp Asp Gly Leu Gly Leu Gly
465 470 475 480

Leu Val Trp Asn Thr Arg Arg Ile Lys Gly Thr Ile Thr Asp Phe Ala
485 490 495

Leu Ala Asp Met Asn Asn Asp Gly Lys Leu Asp Leu Val Val Ser Val
500 505 510

Asn Ser His Thr Gly Ile Leu Gly Leu Glu Lys Arg Lys Thr Ile Ile
515 520 525

Val Phe Tyr Pro Leu Glu Val Asp Lys Gln Gly Ile Pro Lys Ala Val
530 535 540

Glu Asp Asn
545

<210> 7
<211> 1564
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (41)..(1522)

<400> 7
agaagtatgt tctataagta gagtaaggaa tataaaaaat atg gtt agt tat att 55
Met Val Ser Tyr Ile
1 5

cgt tta tta gga agt ata ttt tta gta tta gca att ttt ggt tgt ggc 103
Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala Ile Phe Gly Cys Gly
10 15 20

gct cag ttt aat aaa ccc tct tta ctt gat gaa acc cct ata gat tac 151
Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu Thr Pro Ile Asp Tyr
25 30 35

Substitute Sequence Listing																
agt Ser	tct Ser	gta Val 40	ctt Leu	tct Ser	gat Asp	tac Tyr	ata Ile 45	gta Val	gaa Glu	tta Leu	gaa Glu 50	aaa Lys	gaa Glu	cca Pro	ctt Leu	199
cag Gln	tat Tyr 55	ata Ile	tta Leu	cta Leu	aaa Lys	aaa Lys 60	gaa Glu	aaa Lys	ttt Phe	tct Ser	caa Gln 65	atg Met	gag Glu	ata Ile	tat Tyr	247
aat Asn 70	tat Tyr	caa Gln	ttc Phe	aca Thr	tca Ser 75	caa Gln	cat His	tgg Trp	tct Ser	cca Pro 80	gat Asp	aat Asn	ttt Phe	gta Val	tca Ser 85	295
cct Pro	gct Ala	ata Ile	tgg Trp	gaa Glu 90	cat His	cag Gln	gta Val	gat Asp	ata Ile 95	tat Tyr	atc Ile	cct Pro	cac His	cat His 100	cca Pro	343
gtt Val	tca Ser	gaa Glu	cgt Arg 105	gca Ala	ctt Leu	ctt Leu	atc Ile 110	atc Ile	aat Asn	aat Asn	ggt Gly	att Ile	aat Asn 115	aat Asn	ggt Gly	391
aca Thr	ttt Phe	ttt Phe 120	act Thr	tct Ser	cct Pro	aaa Lys	gct Ala 125	cca Pro	act Thr	gat Asp	ttt Phe 130	act Thr	cca Pro	gaa Glu	gta Val	439
tta Leu	gaa Glu 135	gaa Glu	atc Ile	gct Ala	cgt Arg	tca Ser 140	aca Thr	aaa Lys	act Thr	gta Val	gtc Val 145	att Ile	gct Ala	cta Leu	agt Ser	487
gat Asp 150	atc Ile	cca Pro	aat Asn	cag Gln	tat Tyr 155	ctt Leu	act Thr	tat Tyr	aga Arg	ggt Gly 160	gac Asp	tgg Trp	aga Arg	ttt Phe	ctt Leu 165	535
aag Lys	gaa Glu	gat Asp	gaa Glu	agt Ser 170	att Ile	gct Ala	atg Met	agt Ser	tgg Trp 175	tct Ser	agt Ser	ttt Phe	tta Leu	caa Gln 180	gat Asp	583
cca Pro	gaa Glu	agt Ser	cgg Arg 185	tac Tyr	aca Thr	aga Arg	cct Pro	ctc Leu 190	tat Tyr	gtc Val	cct Pro	atg Met	gtt Val 195	gca Ala	gca Ala	631
gtt Val	tct Ser	cag Gln 200	gca Ala	atg Met	act Thr	ctt Leu	gca Ala 205	gaa Glu	aag Lys	gag Glu	tta Leu	caa Gln 210	gca Ala	tta Leu	aaa Lys	679
att Ile	aag Lys 215	cat His	ttt Phe	att Ile	gta Val	tct Ser 220	ggt Gly	gtg Val	tca Ser	aag Lys	cgt Arg 225	gga Gly	tgg Trp	aca Thr	aca Thr	727
tgg Trp 230	ctt Leu	tca Ser	gct Ala	att Ile	gct Ala 235	gac Asp	tca Ser	cga Arg	gta Val	gat Asp 240	gct Ala	att Ile	acc Thr	ccg Pro	ttt Phe 245	775
gtt Val	att Ile	gat Asp	gca Ala	ttg Leu 250	aat Asn	act Thr	cgg Arg	aaa Lys	gtc Val 255	ctt Leu	gga Gly	cat His	atg Met	tat Tyr 260	aaa Lys	823
aca Thr	tat Tyr	gga Gly 265	aat Asn	aat Asn	tgg Trp	cct Pro	ata Ile 270	gca Ala	ttt Phe	tat Tyr	cca Pro	tat Tyr 275	tat Tyr	aga Arg	ttt Phe	871
gat Asp	tta Leu	gat Asp 280	aaa Lys	caa Gln	cta Leu	gat Asp	aca Thr 285	gtt Val	cct Pro	ttt Phe	ttc Phe	aat Asn 290	ctt Leu	atg Met	aat Asn	919

Substitute Sequence Listing

att gtt gat cca tat aga tat tta gga aca cca tat aag tct cga ctt Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro Tyr Lys Ser Arg Leu 295 300 305	967
gct atc cct aaa tat att gta aat gca agt gga gat gat ttt tat gtc Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly Asp Asp Phe Tyr Val 310 315 320 325	1015
cct gat aat tca agt ttt tac tat gat gat ctc cct gga gag aaa gca Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu Pro Gly Glu Lys Ala 330 335 340	1063
tta cgt ttt gca cca aac tca aat cat cat ggg ata tta aat ttc aca Leu Arg Phe Ala Pro Asn Ser Asn His His Gly Ile Leu Asn Phe Thr 345 350 355	1111
aaa caa tcg ctt att cct ttt gtg aat aga gta caa aaa ggt att tca Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val Gln Lys Gly Ile Ser 360 365 370	1159
acg cca gtt tta gat att tcc aca gag atg acg gaa cga gtt caa tat Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr Glu Arg Val Gln Tyr 375 380 385	1207
gtg act gtt cgt ttt tct gaa gtt cca gag aag ata gta ctt tgg aaa Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys Ile Val Leu Trp Lys 390 395 400 405	1255
gca gca aat cca gag tca cga gat ttt cgt tat gcc tgt cgt gtt agg Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr Ala Cys Arg Val Arg 410 415 420	1303
tac atg gaa aca cca tta cac ctt tct gca aca ggg gaa gtt agc gtt Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr Gly Glu Val Ser Val 425 430 435	1351
tca tta gag atc cct tct gta gga tgg caa gct gct ttt att gaa gct Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala Ala Phe Ile Glu Ala 440 445 450	1399
aca ttt aaa gat ggt ttt gtt gca aca aca cca gtg tat att tta cca Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro Val Tyr Ile Leu Pro 455 460 465	1447
aaa gat ata tat cca cct ata aaa ata cca cct gta cat gga tta tta Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro Val His Gly Leu Leu 470 475 480 485	1495
tgt aag ttt gta cat ggt cga acc tag taactagtag ttgttgtagt Cys Lys Phe Val His Gly Arg Thr 490	1542
gataatctaa aaggatatag at	1564

<210> 8
 <211> 493
 <212> PRT
 <213> Lawsonia intracellularis
 <400> 8

Substitute Sequence Listing

Met Val Ser Tyr Ile Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala
1 5 10 15

Ile Phe Gly Cys Gly Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu
20 25 30

Thr Pro Ile Asp Tyr Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu
35 40 45

Glu Lys Glu Pro Leu Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser
50 55 60

Gln Met Glu Ile Tyr Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro
65 70 75 80

Asp Asn Phe Val Ser Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr
85 90 95

Ile Pro His His Pro Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn
100 105 110

Gly Ile Asn Asn Gly Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp
115 120 125

Phe Thr Pro Glu Val Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val
130 135 140

Val Ile Ala Leu Ser Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly
145 150 155 160

Asp Trp Arg Phe Leu Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser
165 170 175

Ser Phe Leu Gln Asp Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val
180 185 190

Pro Met Val Ala Ala Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu
195 200 205

Leu Gln Ala Leu Lys Ile Lys His Phe Ile Val Ser Gly Val Ser Lys
210 215 220

Arg Gly Trp Thr Thr Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp
225 230 235 240

Ala Ile Thr Pro Phe Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu
245 250 255

Substitute Sequence Listing

Gly His Met Tyr Lys Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr
260 265 270

Pro Tyr Tyr Arg Phe Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe
275 280 285

Phe Asn Leu Met Asn Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro
290 295 300

Tyr Lys Ser Arg Leu Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly
305 310 315 320

Asp Asp Phe Tyr Val Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu
325 330 335

Pro Gly Glu Lys Ala Leu Arg Phe Ala Pro Asn Ser Asn His His Gly
340 345 350

Ile Leu Asn Phe Thr Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val
355 360 365

Gln Lys Gly Ile Ser Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr
370 375 380

Glu Arg Val Gln Tyr Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys
385 390 395 400

Ile Val Leu Trp Lys Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr
405 410 415

Ala Cys Arg Val Arg Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr
420 425 430

Gly Glu Val Ser Val Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala
435 440 445

Ala Phe Ile Glu Ala Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro
450 455 460

Val Tyr Ile Leu Pro Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro
465 470 475 480

Val His Gly Leu Leu Cys Lys Phe Val His Gly Arg Thr
485 490

<210> 9
<211> 2096

Substitute Sequence Listing

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (12)..(2096)

<400> 9

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              1              5              10

att ggt agt gga acc gat ttc caa gct atg att gat caa ctt aag aaa      98
Ile Gly Ser Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys
15              20              25

att gag ctt att cct aaa aat aga ctt gta gtt tcc cat gaa caa tgg      146
Ile Glu Leu Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp
30              35              40              45

aca aaa aaa tat aaa gca ttt gaa gag ctt ata aaa aca gtt aaa gat      194
Thr Lys Lys Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp
50              55              60

act gaa gcg tct tta agt aag cta agt tct gtt ggt gct att tta aaa      242
Thr Glu Ala Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys
65              70              75

aaa gaa ggt tct gtt tca aat act tct gtt gca agc gtt aag gca agt      290
Lys Glu Gly Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser
80              85              90

tct gat gca tct gat gga aca cat aca att gat gtg aaa cag ctt gca      338
Ser Asp Ala Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala
95              100              105

aca aac acg att ctt tct aat aat cat att ttt gat tct aaa act gaa      386
Thr Asn Thr Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu
110              115              120              125

agt att aat aat aca ggt tca cct ggt atc ttt gct tat gag tat aaa      434
Ser Ile Asn Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys
130              135              140

ggg gaa cta cat gaa gtt gaa gtt cct cca ggt agt gat ctt gaa tat      482
Gly Glu Leu His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr
145              150              155

ctt gca aca tta ata aac aaa gat tct aat aat cct ggt gtt aaa gca      530
Leu Ala Thr Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala
160              165              170

aac ctt atc aag act ggc gat ggc tat atg ttt agt ctt gaa gga act      578
Asn Leu Ile Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr
175              180              185

gaa act ggt gca aat gcg act tta tct att tca aat aag aca acg ctt      626
Glu Thr Gly Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu
190              195              200              205

cca gac ttt aaa gca tct gtt gct acc agc agt gca tta gct aat ggt      674
Pro Asp Phe Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly

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Substitute Sequence Listing

210	215	220	
gaa gat aca att att aat act tca gga aca act caa caa ttt tct ttt Glu Asp Thr Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe 225 230 235			722
gaa tac aat gga aga aca ttt act ttc gat att cct tca gga aca aca Glu Tyr Asn Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr 240 245 250			770
gca aaa gaa ctc caa aca gct ata aat gaa aat aca aaa aat aca gga Ala Lys Glu Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly 255 260 265			818
gta cgt gca act ttt gaa aaa cat ggc tca gat ata gta ttg caa tta Val Arg Ala Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu 270 275 280 285			866
gaa gga aca gtt cct aat caa caa gtt aaa gta acc gct agc cct act Glu Gly Thr Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr 290 295 300			914
gat ctt gga agt ttc aca tct tcg ggt caa gca ggc tgg aat aaa cgt Asp Leu Gly Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg 305 310 315			962
gat tct caa gat gct att ttt aat att aat ggt tgg gac caa gaa ctt Asp Ser Gln Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu 320 325 330			1010
aca tct tct aca aat gaa ctt aca gaa gtt atc cca gga ctt caa att Thr Ser Ser Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile 335 340 345			1058
aca cta ctt tcc gaa ggg aaa aca caa att aca att cag act tct act Thr Leu Leu Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr 350 355 360 365			1106
gac gaa gta aaa aaa caa gtt gag aaa gca gta gag tct ata aat aat Asp Glu Val Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn 370 375 380			1154
gtt ctt tcc aaa att caa gag tta act aaa gca aca gct gaa gac aaa Val Leu Ser Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys 385 390 395			1202
gat gat agt aaa gac act tct agt tct tca agt aaa att cca tca tat Asp Asp Ser Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr 400 405 410			1250
tta caa agt cct aca aaa gtg aag gct gga cta ttt aca ggt gat act Leu Gln Ser Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr 415 420 425			1298
ggc ata caa atg ctt agt act aga ctt aag tct atc ttt tct tct aat Gly Ile Gln Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn 430 435 440 445			1346
ggt cta ggt ttt tct cct aaa caa aca caa gat ggt cca ggg gat cta Gly Leu Gly Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu 450 455 460			1394
ttt tca tca ctt gct tca att ggt att gtc gta gat gct gat gag ggt Page 20			1442

Substitute Sequence Listing															
Phe	Ser	Ser	Leu	Ala	Ser	Ile	Gly	Ile	Val	Val	Asp	Ala	Asp	Glu	Gly
			465					470					475		
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Ser	Glu	Thr	Phe	Gly	Gln	Leu	Lys	Ile	Leu	Asp	Arg	Glu	Thr	Ile	Gly
		480					485					490			1490
cct	gat	gca	cct	tat	aca	act	ctt	gat	gag	gca	tta	aaa	aaa	gat	cca
Pro	Asp	Ala	Pro	Tyr	Thr	Thr	Leu	Asp	Glu	Ala	Leu	Lys	Lys	Asp	Pro
	495					500					505				1538
caa	gca	gta	gca	gat	ata	tta	gct	ggt	agt	tct	gga	ata	tct	gat	tca
Gln	Ala	Val	Ala	Asp	Ile	Leu	Ala	Gly	Ser	Ser	Gly	Ile	Ser	Asp	Ser
510					515					520					1586
aca	gat	ttt	tct	tat	caa	gat	cat	att	gtt	gga	aaa	aca	caa	gct	ggt
Thr	Asp	Phe	Ser	Tyr	Gln	Asp	His	Ile	Val	Gly	Lys	Thr	Gln	Ala	Gly
				530					535					540	1634
aca	tat	gat	gta	aag	tat	tct	gta	gat	gca	agt	ggt	act	ata	gga	gac
Thr	Tyr	Asp	Val	Lys	Tyr	Ser	Val	Asp	Ala	Ser	Gly	Thr	Ile	Gly	Asp
			545					550					555		1682
gtt	tac	att	gga	ggt	gta	aaa	gct	tct	cta	tct	gat	cct	gca	aaa	aat
Val	Tyr	Ile	Gly	Gly	Val	Lys	Ala	Ser	Leu	Ser	Asp	Pro	Ala	Lys	Asn
		560					565					570			1730
ata	tat	acg	gtc	aca	tct	ggt	cct	gct	aca	ggt	ctt	agt	ata	gca	gtt
Ile	Tyr	Thr	Val	Thr	Ser	Gly	Pro	Ala	Thr	Gly	Leu	Ser	Ile	Ala	Val
	575					580					585				1778
aat	aat	cgt	act	cca	ggt	atc	aat	gta	gaa	agt	act	gta	aga	gtc	aaa
Asn	Asn	Arg	Thr	Pro	Gly	Ile	Asn	Val	Glu	Ser	Thr	Val	Arg	Val	Lys
590					595					600					1826
caa	ggt	aaa	ctt	agc	caa	ata	caa	gaa	gca	ctt	aaa	gct	gaa	gta	cag
Gln	Gly	Lys	Leu	Ser	Gln	Ile	Gln	Glu	Ala	Leu	Lys	Ala	Glu	Val	Gln
				610					615					620	1874
caa	gat	cct	tta	aaa	gaa	aac	aca	ggt	cct	tta	att	atc	atg	caa	gat
Gln	Asp	Pro	Leu	Lys	Glu	Asn	Thr	Gly	Pro	Leu	Ile	Ile	Met	Gln	Asp
			625					630					635		1922
aac	tat	aag	gat	gtt	atg	aaa	aat	ctt	gag	aca	aga	ata	gaa	aaa	gaa
Asn	Tyr	Lys	Asp	Val	Met	Lys	Asn	Leu	Glu	Thr	Arg	Ile	Glu	Lys	Glu
		640					645					650			1970
aca	caa	aga	gtt	act	agt	tgg	gaa	cgt	atg	atg	cgt	tta	aaa	ttt	tct
Thr	Gln	Arg	Val	Thr	Ser	Trp	Glu	Arg	Met	Met	Arg	Leu	Lys	Phe	Ser
		655				660					665				2018
aga	ctt	gat	gct	gta	tta	gca	aaa	tat	aat	cag	atg	atg	tca	gca	aat
Arg	Leu	Asp	Ala	Val	Leu	Ala	Lys	Tyr	Asn	Gln	Met	Met	Ser	Ala	Asn
670					675					680					2066
gct	tct	agt	tta	ggg	caa	ctt	ggt	gca	taa						
Ala	Ser	Ser	Leu	Gly	Gln	Leu	Gly	Ala							2096
				690											

<210> 10
 <211> 694
 <212> PRT

Substitute Sequence Listing

<213> Lawsonia intracellularis

<400> 10

Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly Ile Gly Ser
1 5 10 15

Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys Ile Glu Leu
20 25 30

Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp Thr Lys Lys
35 40 45

Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp Thr Glu Ala
50 55 60

Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys Lys Glu Gly
65 70 75 80

Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser Ser Asp Ala
85 90 95

Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala Thr Asn Thr
100 105 110

Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu Ser Ile Asn
115 120 125

Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys Gly Glu Leu
130 135 140

His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr Leu Ala Thr
145 150 155 160

Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala Asn Leu Ile
165 170 175

Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr Glu Thr Gly
180 185 190

Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu Pro Asp Phe
195 200 205

Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly Glu Asp Thr
210 215 220

Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe Glu Tyr Asn
225 230 235 240

Substitute Sequence Listing

Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr Ala Lys Glu
245 250 255

Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly Val Arg Ala
260 265 270

Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu Glu Gly Thr
275 280 285

Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr Asp Leu Gly
290 295 300

Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg Asp Ser Gln
305 310 315 320

Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu Thr Ser Ser
325 330 335

Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile Thr Leu Leu
340 345 350

Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr Asp Glu Val
355 360 365

Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn Val Leu Ser
370 375 380

Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys Asp Asp Ser
385 390 395 400

Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr Leu Gln Ser
405 410 415

Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr Gly Ile Gln
420 425 430

Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn Gly Leu Gly
435 440 445

Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu Phe Ser Ser
450 455 460

Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly Ser Glu Thr
465 470 475 480

Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly Pro Asp Ala
485 490 495

Substitute Sequence Listing

Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro Gln Ala Val
500 505 510

Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser Thr Asp Phe
515 520 525

Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly Thr Tyr Asp
530 535 540

Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp Val Tyr Ile
545 550 555 560

Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn Ile Tyr Thr
565 570 575

Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val Asn Asn Arg
580 585 590

Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys Gln Gly Lys
595 600 605

Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln Gln Asp Pro
610 615 620

Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp Asn Tyr Lys
625 630 635 640

Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu Thr Gln Arg
645 650 655

Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser Arg Leu Asp
660 665 670

Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn Ala Ser Ser
675 680 685

Leu Gly Gln Leu Gly Ala
690

<210> 11
<211> 1200
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (13)..(1200)

Substitute Sequence Listing

<400> 11

taggagatag tt atg gct aat gtt agt gga atc cct gca cca cga tta ctt 51
Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu
1 5 10

tcc aca aca aat caa atg acc aat gca gct gct ggt aat act aat aga 99
Ser Thr Thr Asn Gln Met Thr Asn Ala Ala Ala Gly Asn Thr Asn Arg
15 20 25

gct acc ggt agt atg aac ggt cgt aat ctcaca caa ata aaaaca cct 147
Ala Thr Gly Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro
30 35 40 45

cag tcc atg att gat aat gct tca gaa gaa tta aca act tct ctt gaa 195
Gln Ser Met Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu
50 55 60

tct aaa agc agt gac gac ttt gca att aaa gat cgt aaa aga caa ggg 243
Ser Lys Ser Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly

aaa gga tct gat tct cta tta aaa atg gtt caa gaa tat aca gag ctg 291
Lys Gly Ser Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu
80 85 90

acg aat gat gat acc cgt aat gct aaa aga gct atg tta tcc cag gta 339
Thr Asn Asp Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val
95 100 105

tta cgt gca agt caa agt tca caa gat gta ctc gaa aaa aca tta gaa 387
Leu Arg Ala Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu
110 115 120 125

caa ttt tct aat aaa aca gat gct tgg gct tct ctt gca gaa att gca 435
Gln Phe Ser Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala
130 135 140

caa gaa tat ggt gca gaa tct cca cag cca aca gga tta aaa tct gta 483
Gln Glu Tyr Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val
145 150 155

tta gat gct atg gag aca tta gaa aat gag ttt ggt gat gaa att aaa 531
Leu Asp Ala Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys
160 165 170

gca gga cta aaa gga gct cta aat tca aaa gaa ttt act gat ata ggc 579
Ala Gly Leu Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly
175 180 185

agt gca gca cag tta aga gat ctt tat aca aca aca gta act ata aca 627
 Ser Ala Ala Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr
 190 195 200 205

gct gca cct gat gca gtg tta gca aga ctt ctt gaa gaa tat gag agt 675
Ala Ala Pro Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser
210 215 220

gat gat gat ctg gat aga gcc att gat ttc ctt cta tct aca ctt ggt 723
Asp Asp Asp Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly
225 230 235

gga gag ctt gaa tca gct gat cca agt atg gat aaa gta cat ctt caa 771
Page 25

Substitute Sequence Listing																
Gly	Glu	Leu	Glu	Ser	Ala	Asp	Pro	Ser	Met	Asp	Lys	Val	His	Leu	Gln	
		240					245					250				
agt	gta	atg	ggt	gat	att	gaa	aaa	aca	caa	caa	ctt	cat	agc	tct	cat	819
Ser	Val	Met	Gly	Asp	Ile	Glu	Lys	Thr	Gln	Gln	Leu	His	Ser	Ser	His	
	255					260					265					
aaa	caa	tgt	act	aca	gcc	ctt	agc	agg	tgg	aaa	gag	aaa	cat	aaa	ggt	867
Lys	Gln	Cys	Thr	Thr	Ala	Leu	Ser	Arg	Trp	Lys	Glu	Lys	His	Lys	Gly	
270					275					280					285	
ggg	ggg	gaa	aat	agt	aca	cta	act	cct	tta	gaa	atg	atg	cgt	gaa	cta	915
Gly	Gly	Glu	Asn	Ser	Thr	Leu	Thr	Pro	Leu	Glu	Met	Met	Arg	Glu	Leu	
				290					295					300		
att	gca	cta	aaa	aat	gaa	aat	ttt	att	tct	cct	tcc	tct	ata	gat	aaa	963
Ile	Ala	Leu	Lys	Asn	Glu	Asn	Phe	Ile	Ser	Pro	Ser	Ser	Ile	Asp	Lys	
			305					310					315			
att	gtt	gat	caa	gct	gat	ccc	caa	gat	att	gaa	aaa	gaa	gtc	ctt	ttt	1011
Ile	Val	Asp	Gln	Ala	Asp	Pro	Gln	Asp	Ile	Glu	Lys	Glu	Val	Leu	Phe	
		320				325						330				
tta	caa	gag	atg	tta	gct	gct	gta	aga	aaa	ttt	ccc	att	atg	gta	ttt	1059
Leu	Gln	Glu	Met	Leu	Ala	Ala	Val	Arg	Lys	Phe	Pro	Ile	Met	Val	Phe	
	335				340						345					
gat	aat	gtc	gaa	aat	cgt	gta	aga	gtt	atg	ggt	gct	gta	caa	gat	gct	1107
Asp	Asn	Val	Glu	Asn	Arg	Val	Arg	Val	Met	Gly	Ala	Val	Gln	Asp	Ala	
350					355					360					365	
gtt	gac	gat	gct	gta	aga	aga	gaa	gat	gaa	ttc	ctc	ttt	caa	aaa	gaa	1155
Val	Asp	Asp	Ala	Val	Arg	Arg	Glu	Asp	Glu	Phe	Leu	Phe	Gln	Lys	Glu	
			370						375					380		
cat	cct	gat	gta	cca	cta	caa	cca	gat	gaa	aat	aat	ata	caa	taa		1200
His	Pro	Asp	Val	Pro	Leu	Gln	Pro	Asp	Glu	Asn	Asn	Ile	Gln			
			385					390					395			

<210> 12
 <211> 395
 <212> PRT
 <213> Lawsonia intracellularis

<400> 12

Met	Ala	Asn	Val	Ser	Gly	Ile	Pro	Ala	Pro	Arg	Leu	Leu	Ser	Thr	Thr
1				5					10					15	
Asn	Gln	Met	Thr	Asn	Ala	Ala	Ala	Gly	Asn	Thr	Asn	Arg	Ala	Thr	Gly
			20					25					30		
Ser	Met	Asn	Gly	Arg	Asn	Leu	Thr	Gln	Ile	Lys	Thr	Pro	Gln	Ser	Met
		35				40						45			
Ile	Asp	Asn	Ala	Ser	Glu	Glu	Leu	Thr	Thr	Ser	Leu	Glu	Ser	Lys	Ser
	50					55					60				

Substitute Sequence Listing

Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly Lys Gly Ser
65 70 75 80

Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu Thr Asn Asp
85 90 95

Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val Leu Arg Ala
100 105 110

Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu Gln Phe Ser
115 120 125

Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala Gln Glu Tyr
130 135 140

Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val Leu Asp Ala
145 150 155 160

Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys Ala Gly Leu
165 170 175

Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly Ser Ala Ala
180 185 190

Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr Ala Ala Pro
195 200 205

Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser Asp Asp Asp
210 215 220

Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly Gly Glu Leu
225 230 235 240

Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln Ser Val Met
245 250 255

Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His Lys Gln Cys
260 265 270

Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly Gly Gly Glu
275 280 285

Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu Ile Ala Leu
290 295 300

Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys Ile Val Asp
305 310 315 320

Substitute Sequence Listing

Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe Leu Gln Glu
325 330 335

Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe Asp Asn Val
340 345 350

Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala Val Asp Asp
355 360 365

Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu His Pro Asp
370 375 380

Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln
385 390 395

<210> 13
<211> 1269
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (32)..(1222)

<400> 13
tgttggaaat tctctctgga ggagtaaagc a atg aca aat ttt gga gat ata 52
Met Thr Asn Phe Gly Asp Ile
1 5

agc gga agc tcc gca aga atg agt agc ttg atg act ggt aca tcc ggt 100
Ser Gly Ser Ser Ala Arg Met Ser Ser Leu Met Thr Gly Thr Ser Gly
10 15 20

gaa gaa gga ctt gaa gaa ctt gaa ggt ggt gtt cct aaa gag caa ggt 148
Glu Glu Gly Leu Glu Glu Leu Glu Gly Gly Val Pro Lys Glu Gln Gly
25 30 35

ggt cca ggt aaa gga gat gct tca gag gct gct aaa ggt caa gca gca 196
Gly Pro Gly Lys Gly Asp Ala Ser Glu Ala Ala Lys Gly Gln Ala Ala
40 45 50 55

gca gat agt att aat tca gct ggt ggt act gaa aag cct gga gaa gtt 244
Ala Asp Ser Ile Asn Ser Ala Gly Gly Thr Glu Lys Pro Gly Glu Val
60 65 70

ggt gat aag gaa gat gta ggg gaa ggt ggc gaa ata cct gaa ggt ggt 292
Gly Asp Lys Glu Asp Val Gly Glu Gly Gly Glu Ile Pro Glu Gly Gly
75 80 85

gaa ata cct gag ggt ggt gaa gaa gtt cca gag gaa ccc cca tat gtc 340
Glu Ile Pro Glu Gly Gly Glu Glu Val Pro Glu Glu Pro Pro Tyr Val
90 95 100

cct cct cca ttg gtt gaa cca gct aaa atc agt aca gta aca gat ctc 388
Pro Pro Pro Leu Val Glu Pro Ala Lys Ile Ser Thr Val Thr Asp Leu
105 110 115

Substitute Sequence Listing

agt Ser 120	acg Thr	tta Leu	atg Met	gga Gly 125	tca Ser 125	cta Leu	cag Gln	ctg Leu	aca Thr	gag Glu 130	caa Gln	aaa Lys	aag Lys	aat Asn	gct Ala 135	436
gaa Glu	aaa Lys	aca Thr	gta Val	aat Asn 140	gaa Glu	att Ile	aaa Lys	gca Ala	cag Gln 145	aat Asn	aaa Lys	gag Glu	caa Gln	caa Gln 150	gta Val	484
aag Lys	ttc Phe	caa Gln	gag Glu 155	caa Gln	att Ile	aaa Lys	aag Lys	att Ile 160	gag Glu	gat Asp	aat Asn	att Ile	gct Ala 165	gaa Glu	tct Ser	532
aag Lys	aaa Lys	agt Ser 170	ggt Gly	ata Ile	ctt Leu	aag Lys	ttt Phe 175	ttc Phe	caa Gln	aag Lys	ttg Leu	ttt Phe 180	gca Ala	ggt Val	att Ile	580
ggt Gly 185	gct Ala	gta Val	cta Leu	gga Gly	gct Ala	att Ile 190	gga Gly	ggt Gly	gcg Ala	cta Leu	gct Ala 195	att Ile	gct Ala	gca Ala	ggt Gly	628
gct Ala 200	gct Ala	tca Ser	ggt Gly	aac Asn	cca Pro 205	tta Leu	ttg Leu	gtt Val	gct Ala	gca Ala 210	ggt Gly	att Ile	atg Met	gct Ala	att Ile 215	676
gta Val	gct Ala	tca Ser	att Ile	gat Asp 220	gca Ala	gca Ala	atg Met	tcg Ser	tcg Ser 225	cta Leu	tcg Ser	gat Asp	ggt Gly	aaa Lys 230	gtg Val	724
tcc Ser	atc Ile	tca Ser	gca Ala 235	ggg Gly	att Ile	agt Ser	aag Lys	gct Ala 240	ctt Leu	gag Glu	gct Ala	atg Met	gga Gly 245	gta Val	cca Pro	772
gca Ala	gaa Glu	aca Thr 250	gca Ala	caa Gln	tgg Trp	att Ile	gca Ala 255	ttt Phe	ggt Gly	ata Ile	cag Gln	tta Leu 260	gca Ala	atg Met	att Ile	820
gca Ala 265	gtg Val	act Thr	ata Ile	gct Ala	att Ile	ggt Gly 270	ttt Phe	gcc Ala	tct Ser	ggt Gly	ggt Gly 275	ggt Gly	gga Gly	gca Ala	atg Met	868
gct Ala 280	gga Gly	gtg Val	tca Ser	aaa Lys	ata Ile 285	gca Ala	gat Asp	atg Met	ttt Phe	tca Ser 290	aag Lys	tct Ser	caa Gln	gat Asp	gta Val 295	916
gct Ala	aag Lys	ttg Leu	gca Ala	cag Gln 300	atg Met	att Ile	gaa Glu	aaa Lys	gct Ala 305	tct Ser	aaa Lys	ata Ile	gta Val	caa Gln 310	atc Ile	964
gct Ala	ggt Gly	tca Ser	gtt Val 315	aat Asn	cag Gln	tct Ser	gct Ala	ata Ile 320	ggc Gly	ggt Gly	aca Thr	ggt Gly	att Ile 325	ggt Gly	aca Thr	1012
gct Ala	gta Val	gtg Val 330	caa Gln	agc Ser	aat Asn	ata Ile	aaa Lys 335	gct Ala	aat Asn	gaa Glu	tct Ser	gaa Glu 340	caa Gln	aaa Lys	gaa Glu	1060
att Ile 345	gaa Glu	gct Ala	gct Ala	att Ile	gca Ala	aaa Lys 350	gtt Val	aaa Lys	gct Ala	aag Lys	ata Ile 355	gag Glu	acg Thr	tta Leu	caa Gln	1108
gac Asp	ttc Phe	ttt Phe	aaa Lys	aac Asn	caa Gln	atg Met	gaa Glu	caa Gln	ttc Phe	aat Asn	gct Ala	ata Ile	atg Met	aaa Lys	ata Ile	1156

Substitute Sequence Listing

360		365		370		375	
ata aca gat att att	caa gat agc gtc	aat aca aaa ata gct gtt	caa	1204			
Ile Thr Asp Ile	Ile Gln Asp Ser Val	Asn Thr Lys Ile Ala Val	Gln				
	380	385	390				
cgt ggt gca cgt gag	taa tacctttagt aaatacagtg	actatactat	1252				
Arg Gly Ala Arg	Glu						
	395						
aatatataaa ttaataa			1269				
<210>	14						
<211>	396						
<212>	PRT						
<213>	Lawsonia intracellularis						
<400>	14						
Met Thr Asn Phe	Gly Asp Ile Ser Gly	Ser Ser Ala Arg Met	Ser Ser				
1	5	10	15				
Leu Met Thr	Gly Thr Ser Gly Glu	Glu Gly Leu Glu Glu	Leu Glu Gly				
	20	25	30				
Gly Val	Pro Lys Glu Gln Gly	Gly Pro Gly Lys Gly	Asp Ala Ser Glu				
	35	40	45				
Ala Ala Lys Gly Gln Ala	Ala Ala Asp Ser Ile	Asn Ser Ala Gly Gly					
	50	55	60				
Thr Glu Lys Pro Gly	Glu Val Gly Asp Lys	Glu Asp Val Gly Glu Gly					
65	70	75	80				
Gly Glu Ile Pro	Glu Gly Gly Glu Ile	Pro Glu Gly Gly Glu	Glu Val				
	85	90	95				
Pro Glu Glu	Pro Tyr Val Pro	Pro Pro Leu Val	Glu Pro Ala Lys				
	100	105	110				
Ile Ser Thr	Val Thr Asp Leu	Ser Thr Leu Met Gly	Ser Leu Gln Leu				
	115	120	125				
Thr Glu Gln Lys Lys	Asn Ala Glu Lys Thr	Val Asn Glu Ile Lys Ala					
	130	135	140				
Gln Asn Lys Glu Gln	Gln Val Lys Phe Gln	Glu Gln Ile Lys Lys	Ile				
145	150	155	160				
Glu Asp Asn Ile	Ala Glu Ser Lys Lys	Ser Gly Ile Leu Lys	Phe Phe				
	165	170	175				

Substitute Sequence Listing

Gln Lys Leu Phe Ala Val Ile Gly Ala Val Leu Gly Ala Ile Gly Gly
180 185 190

Ala Leu Ala Ile Ala Ala Gly Ala Ala Ser Gly Asn Pro Leu Leu Val
195 200 205

Ala Ala Gly Ile Met Ala Ile Val Ala Ser Ile Asp Ala Ala Met Ser
210 215 220

Ser Leu Ser Asp Gly Lys Val Ser Ile Ser Ala Gly Ile Ser Lys Ala
225 230 235 240

Leu Glu Ala Met Gly Val Pro Ala Glu Thr Ala Gln Trp Ile Ala Phe
245 250 255

Gly Ile Gln Leu Ala Met Ile Ala Val Thr Ile Ala Ile Gly Phe Ala
260 265 270

Ser Gly Gly Gly Gly Ala Met Ala Gly Val Ser Lys Ile Ala Asp Met
275 280 285

Phe Ser Lys Ser Gln Asp Val Ala Lys Leu Ala Gln Met Ile Glu Lys
290 295 300

Ala Ser Lys Ile Val Gln Ile Ala Gly Ser Val Asn Gln Ser Ala Ile
305 310 315 320

Gly Gly Thr Gly Ile Gly Thr Ala Val Val Gln Ser Asn Ile Lys Ala
325 330 335

Asn Glu Ser Glu Gln Lys Glu Ile Glu Ala Ala Ile Ala Lys Val Lys
340 345 350

Ala Lys Ile Glu Thr Leu Gln Asp Phe Phe Lys Asn Gln Met Glu Gln
355 360 365

Phe Asn Ala Ile Met Lys Ile Ile Thr Asp Ile Ile Gln Asp Ser Val
370 375 380

Asn Thr Lys Ile Ala Val Gln Arg Gly Ala Arg Glu
385 390 395

<210> 15
<211> 894
<212> DNA
<213> Lawsonia intracellularis

Substitute Sequence Listing

<220>

<221> CDS

<222> (13)..(894)

<400> 15

aggaggaatt at atg tct ctt gtc att aat aac aac ctg atg gcc gtc aat 51
Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn

1

5

10

gct caa cgt aac tta agc aag tct tat gga gaa ctg agt tct tct gtt 99
Ala Gln Arg Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val

15

20

25

cga aaa ctt tct tca ggt ctt cgt gta gga act gct gct gat gac tca 147
Arg Lys Leu Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser

30

35

40

45

gca ggg tta gcc att cga gaa ctc atg aga tct gac att gca aca aca 195
Ala Gly Leu Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr

50

55

60

caa caa gga ata cga aat gcg aat gat gct att tct atg att caa act 243
Gln Gln Gly Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr

65

70

75

gcg gat ggt gca ctt gga gtc atc gat gaa aag ctc att cga atg aaa 291
Ala Asp Gly Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys

80

85

90

gaa ctt gct gaa caa gct gct aca ggt aca tat aac tcc act cag cgt 339
Glu Leu Ala Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg

95

100

105

atg att att gac tct gaa tat caa gct atg gcc tca gaa att act cgt 387
Met Ile Ile Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg

110

115

120

125

att gct aat gcg aca gaa ttt aat ggt ata aaa ctt ctt gat ggt tca 435
Ile Ala Asn Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser

130

135

140

tta tca ggt aat cat gat ggg aaa aaa ata aat tca act ggt gca gta 483
Leu Ser Gly Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val

145

150

155

cgt atc cac ttt ggg aca tct aac agc tct gct gaa gat tac tat gat 531
Arg Ile His Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp

160

165

170

att aaa att ggt ggc tct aca gct tct gca tta gga ctt ggt aat aca 579
Ile Lys Ile Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr

175

180

185

gta aaa ggt gcg ggt gct aca gtc tct act caa gct gca gca caa aat 627
Val Lys Gly Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn

190

195

200

205

gcc tta aaa gct ata gat aat gcc att gtt tca aaa gat aaa att cga 675
Ala Leu Lys Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg

210

215

220

gca cac ctt ggt gga tta caa aat aga ctt gaa gct aca gtt gat aat 723
Ala His Leu Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn

Substitute Sequence Listing

225	230	235	
tta agt ata caa aat gaa aac tta caa gct gct gaa tct cgt ata tct Leu Ser Ile Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser 240 245 250			771
gat ata gat gta agc caa gaa atg aca caa ttt gta cgt aac caa ata Asp Ile Asp Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile 255 260 265			819
ctt aca caa aca ggt gtt gct atg ctt tca caa gct aat tct cta cca Leu Thr Gln Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro 270 275 280 285			867
cgt atg gct cag caa ctt att ggc taa Arg Met Ala Gln Gln Leu Ile Gly 290			894

<210> 16
 <211> 293
 <212> PRT
 <213> Lawsonia intracellularis
 <400> 16

Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn Ala Gln Arg
 1 5 10 15

Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val Arg Lys Leu
 20 25 30

Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser Ala Gly Leu
 35 40 45

Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr Gln Gln Gly
 50 55 60

Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr Ala Asp Gly
 65 70 75 80

Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys Glu Leu Ala
 85 90 95

Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg Met Ile Ile
 100 105 110

Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg Ile Ala Asn
 115 120 125

Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser Leu Ser Gly
 130 135 140

Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val Arg Ile His

145 150 155 160

Gln Gln Leu Ile Gly
290

aga acc gaa acc tta atc aat gta aac aaa cca ttt gat tct ttt ttt 196

Substitute Sequence Listing																
Arg	Thr	Glu	Thr	Leu 45	Ile	Asn	Val	Asn	Lys 50	Pro	Phe	Asp	Ser	Phe 55	Phe	
gga Gly	ggt Gly	tct Ser	gac Asp 60	tct Ser	aca Thr	ata Ile	gga Gly	acc Thr 65	ctt Leu	gaa Glu	aca Thr	gga Gly	cct Pro 70	act Thr	aat Asn	244
ctt Leu	acc Thr	ttc Phe 75	aca Thr	aca Thr	gta Val	gga Gly	gcc Ala 80	ttc Phe	cgc Arg	aat Asn	tct Ser	gtt Val 85	ttc Phe	aga Arg	att Ile	292
att Ile	ggt Gly 90	ggt Gly	ggt Gly	agg Arg	tct Ser	agt Ser 95	ttt Phe	aac Asn	aac Asn	cca Pro	aat Asn 100	aca Thr	gtt Val	aaa Lys	ggc Gly	340
aat Asn 105	ggt Val	act Thr	cta Leu	act Thr	ggt Val 110	tat Tyr	aat Asn	act Thr	gat Asp	gta Val 115	gaa Glu	aga Arg	ata Ile	att Ile	ggt Gly 120	388
gca Ala	ggt Gly	atc Ile	agc Ser	aat Asn 125	aga Arg	gga Gly	ctt Leu	gta Val	acc Thr 130	ggt Val	act Thr	ggc Gly	tca Ser	gta Val 135	aat Asn	436
atg Met	aag Lys	cta Leu	gaa Glu 140	aat Asn	ggt Val	tct Ser	ggt Val	act Thr 145	aga Arg	gga Gly	att Ile	tat Tyr	ggt Gly 150	ggt Gly	gtc Val	484
tat Tyr	act Thr	caa Gln 155	aat Asn	gga Gly	cat His	gta Val	cta Leu 160	ggc Gly	tct Ser	atc Ile	aac Asn	atg Met 165	cat His	ttg Leu	aaa Lys	532
aac Asn 170	gtc Val	caa Gln	act Thr	cca Pro	cta Leu	tta Leu 175	ata Ile	ggt Gly	tct Ser	gga Gly	gta Val 180	agc Ser	aat Asn	gga Gly	cct Pro	580
aat Asn 185	cgt Arg	att Ile	act Thr	gta Val	aat Asn 190	gga Gly	gac Asp	ata Ile	aac Asn	att Ile 195	gat Asp	ggt Val	gaa Glu	gac Asp	tct Ser 200	628
agg Arg	att Ile	caa Gln	tat Tyr	gta Val 205	aac Asn	att Ile	aca Thr	gga Gly	gaa Glu 210	gta Val	gat Asp	gca Ala	ggg Gly	ata Ile 215	aaa Lys	676
gga Gly	aat Asn	gct Ala	act Thr 220	cta Leu	act Thr	gta Val	aaa Lys	aaa Lys 225	tct Ser	act Thr	ggt Val	gag Glu	ctt Leu 230	ata Ile	aac Asn	724
tct Ser	ggt Gly	aga Arg 235	ggt Gly	aat Asn	atc Ile	tta Leu	ggt Gly 240	aat Asn	ctc Leu	aaa Lys	ata Ile	tct Ser 245	ata Ile	gca Ala	gat Asp	772
tca Ser	aat Asn 250	ata Ile	agg Arg	ggg Gly	tta Leu	tca Ser 255	cca Pro	gta Val	gac Asp	ttt Phe	ggt Gly 260	tct Ser	tca Ser	gta Val	tat Tyr	820
ggg Gly 265	gac Asp	aca Thr	tct Ser	ata Ile	aat Asn 270	gta Val	att Ile	aat Asn	tct Ser	cag Gln 275	att Ile	aat Asn	gat Asp	att Ile	act Thr 280	868
ctt Leu	ata Ile	cca Pro	agg Arg	gct Ala 285	ggt Gly	gga Gly	atg Met	ctt Leu	gta Val 290	ggt Gly	cct Pro	ggt Val	acc Thr	cta Leu 295	gat Asp	916

Substitute Sequence Listing																
atc Ile	aca Thr	agc Ser	agt Ser 300	act Thr	ata Ile	caa Gln	aat Asn 305	ata Ile 305	caa Gln	tgt Cys	ggg Gly	cct Pro	gtc Val 310	agt Ser	caa Gln	964
aat Asn	aat Asn	caa Gln 315	ctt Leu	aac Asn	aca Thr	cta Leu	aat Asn 320	gta Val	act Thr	gtt Val	aat Asn	act Thr 325	agt Ser	aac Asn	att Ile	1012
act Thr	aac Asn 330	tta Leu	aac Asn	ctt Leu	ggt Gly 335	agt Ser 335	gtc Val	gaa Glu	ggt Gly	cat His	aca Thr 340	ata Ile	tca Ser	act Thr	aca Thr	1060
gca Ala 345	act Thr	gtt Val	act Thr	gat Asp	agt Ser 350	aat Asn	att Ile	act Thr	aac Asn	ctt Leu 355	aat Asn	gtc Val	gga Gly	acc Thr	ttc Phe 360	1108
aat Asn	gga Gly	ctt Leu	gga Gly	gta Val 365	act Thr	gag Glu	aat Asn	gcc Ala	tct Ser 370	gta Val	atc Ile	att Ile	aat Asn	agt Ser 375	ggc Gly	1156
aat Asn	att Ile	act Thr	aac Asn 380	ctt Leu	aat Asn	gtc Val	gga Gly 385	act Thr 385	aat Asn	gta Val	ata Ile	gct Ala	gca Ala 390	gcc Ala	aca Thr	1204
act Thr	att Ile	aat Asn 395	tcc Ser	tct Ser	gcg Ala	acc Thr	ata Ile 400	cac His	gac Asp	gga Gly	ctt Leu	att Ile 405	gca Ala	aac Asn	ctt Leu	1252
acc Thr	tta Leu 410	ggc Gly	tca Ser	caa Gln	ggt Gly	aat Asn 415	ggt Gly	cgt Arg	act Thr	atg Met	ata Ile 420	gct Ala	aca Thr	gca Ala	aat Asn	1300
gtt Val 425	aat Asn	ggt Gly	gga Gly	act Thr	att Ile 430	gga Gly	tta Leu	tta Leu	act Thr	atg Met 435	ggt Gly	tca Ser	gaa Glu	aac Asn	ttc Phe 440	1348
ata Ile	cca Pro	ggc Gly	aca Thr	aga Arg 445	cca Pro	att Ile	act Thr	gaa Glu	tta Leu 450	gca Ala	ata Ile	cta Leu	aac Asn	atg Met 455	tct Ser	1396
ggt Gly	gga Gly	tta Leu	att Ile 460	gaa Glu	aga Arg	att Ile	atc Ile	gta Val 465	ggt Gly	aat Asn	gcc Ala	aac Asn	tct Ser 470	tca Ser	acc Thr	1444
ata Ile	aac Asn	ttt Phe 475	act Thr	cct Pro	ggg Gly	aag Lys	aga Arg 480	tca Ser	att Ile	gta Val	aaa Lys	aca Thr 485	ata Ile	aat Asn	ggt Gly	1492
cca Pro	gaa Glu 490	ctt Leu	cca Pro	tat Tyr	tta Leu	gtt Val 495	aac Asn	ata Ile	caa Gln	aaa Lys	ggt Gly 500	gct Ala	atg Met	aca Thr	caa Gln	1540
tgg Trp 505	ggc Gly	act Thr	aaa Lys	aat Asn	atg Met 510	ccc Pro	ttt Phe	tta Leu	ttg Leu	gat Asp 515	aca Thr	aga Arg	aat Asn	tta Leu	atc Ile 520	1588
ttg Leu	tcc Ser	gga Gly	act Thr	ctg Leu 525	att Ile	acc Thr	tca Ser	aat Asn	att Ile 530	caa Gln	cta Leu	gct Ala	gat Asp	tta Leu 535	tct Ser	1636
ata Ile	acc Thr	aat Asn	cta Leu 540	ttt Phe	gtt Val	gct Ala	aat Asn	ggc Gly 545	ggt Gly	aca Thr	cta Leu	gta Val	cct Pro 550	aga Arg	aaa Lys	1684

Substitute Sequence Listing

tta Leu	ata Ile	cct Pro 555	ggg Gly	aac Asn	caa Gln	cct Pro 560	gtt Val	ata Ile	cag Gln	ttt Phe	ctt Leu	gga Gly 565	ggt Gly	cct Pro	caa Gln	1732
tca Ser	ctc Leu 570	tta Leu	gtt Val	atc Ile	cat His	caa Gln 575	cca Pro	tta Leu	aaa Lys	gta Val 580	aat Asn	tta Leu	agc Ser	tta Leu	tca Ser	1780
cca Pro 585	aaa Lys	ctt Leu	att Ile	gga Gly	agt Ser 590	agc Ser	atg Met	gtg Val	cca Pro	ctt Leu 595	gct Ala	ttt Phe	gtc Val	tct Ser	caa Gln 600	1828
tct Ser	ttt Phe	tca Ser	tca Ser	cca Pro 605	gat Asp	ctt Leu	ttt Phe	gtt Val	aaa Lys 610	caa Gln	act Thr	aga Arg	agt Ser	ggt Gly 615	ctc Leu	1876
att Ile	tgg Trp	agt Ser	gat Asp 620	ctt Leu	gag Glu	ttt Phe	gat Asp 625	cca Pro	aca Thr	aca Thr	tct Ser	att Ile	tgg Trp 630	tat Tyr	gtt Val	1924
aat Asn	aat Asn	atc Ile 635	caa Gln	gca Ala	tct Ser	caa Gln	gat Asp 640	ttt Phe	tac Tyr	tct Ser	ttc Phe	tct Ser 645	att Ile	gct Ala	cgt Arg	1972
gag Glu 650	act Thr	act Thr	aac Asn	tgg Trp	cta Leu	aga Arg 655	caa Gln	caa Gln	cat His	ata Ile	tgg Trp 660	act Thr	cta Leu	caa Gln	aac Asn	2020
cgt Arg 665	tca Ser	agt Ser	aaa Lys	ctt Leu	tta Leu 670	gac Asp	aac Asn	gaa Glu	cat His	tat Tyr 675	gga Gly	cta Leu	tgg Trp	ata Ile	aat Asn 680	2068
gtt Val	caa Gln	ggt Gly	gga Gly	cat His 685	gaa Glu	agt Ser	ctt Leu	gat Asp	act Thr 690	tct Ser	att Ile	ggt Gly	agc Ser	aaa Lys 695	gca Ala	2116
aaa Lys	atg Met	cca Pro	tgg Trp 700	ata Ile	atg Met	gca Ala	aca Thr	gca Ala 705	gga Gly	tat Tyr	gac Asp	tat Tyr	ctt Leu 710	caa Gln	caa Gln	2164
cta Leu	cca Pro	agg Arg 715	tta Leu	gat Asp	atg Met	aaa Lys	gcc Ala 720	ctt Leu	tat Tyr	ggt Gly	ctt Leu	gct Ala 725	ttt Phe	ggt Gly	gct Ala	2212
tct Ser	aaa Lys 730	ggt Gly	aaa Lys	agt Ser	aaa Lys	tgg Trp 735	tct Ser	agc Ser	gtc Val	aac Asn	tct Ser 740	aca Thr	aaa Lys	aat Asn	gat Asp	2260
gct Ala 745	gag Glu	cta Leu	ggt Gly	atg Met	gtt Val 750	agt Ser	ggt Gly	tat Tyr	gta Val	ggt Gly 755	ctt Leu	atc Ile	cat His	aac Asn	aaa Lys 760	2308
act Thr	ggg Gly	ctc Leu	tat Tyr	agt Ser 765	aca Thr	ttg Leu	acc Thr	tta Leu	caa Gln 770	ctt Leu	gcg Ala	tct Ser	agt Ser	aaa Lys 775	tta Leu	2356
cat His	act Thr	aat Asn	tct Ser 780	aca Thr	ggg Gly	ttc Phe	tat Tyr	aga Arg 785	aat Asn	ttt Phe	aaa Lys	tgg Trp 790	aca Thr	gaa Glu	aca Thr	2404
act Thr	cca Pro	aca Thr	gaa Glu	gca Ala	ctt Leu	gaa Glu	ctt Leu	gga Gly	tgg Trp	aaa Lys	tac Tyr	act Thr	ttc Phe	aac Asn	aac Asn	2452

Substitute Sequence Listing

795	ggt att aaa atg aat cct cgt gga caa ctt att ttt gaa caa aca tct Gly Ile Lys Met Asn Pro Arg Gly Gln Leu Ile Phe Glu Gln Thr Ser	800	805	2500
	aaa cac cat ttt gat tta gga att caa aat gat aag gct ata tta gat Lys His His Phe Asp Leu Gly Ile Gln Asn Asp Lys Ala Ile Leu Asp			2548
	aaa agc cag tta ata aca agt tct ctt ggt att acc gtt gaa tat aag Lys Ser Gln Leu Ile Thr Ser Ser Leu Gly Ile Thr Val Glu Tyr Lys			2596
	cta cca gtt acc aca cct att aat ctt tat gct ggt att gaa agg ata Leu Pro Val Thr Thr Pro Ile Asn Leu Tyr Ala Gly Ile Glu Arg Ile			2644
	aaa ggt cag tct gga aac ttt gca att agt tcc cag agc ctt caa atg Lys Gly Gln Ser Gly Asn Phe Ala Ile Ser Ser Gln Ser Leu Gln Met			2692
	aag ttc aag cat gac aat gat aca agt gta gtt aga gca aca ata ggt Lys Phe Lys His Asp Asn Asp Thr Ser Val Val Arg Ala Thr Ile Gly			2740
	aca aat ata tta ttg gga gaa cat ttt aat att cac tgt gat ata ttt Thr Asn Ile Leu Leu Gly Glu His Phe Asn Ile His Cys Asp Ile Phe			2788
	gga gat aaa gga aat gat aaa ggc att ggt ggg caa gca gga ttt aca Gly Asp Lys Gly Asn Asp Lys Gly Ile Gly Gly Gln Ala Gly Phe Thr			2836
	tac aaa ttt taa Tyr Lys Phe			2848

<210> 18
 <211> 939
 <212> PRT
 <213> Lawsonia intracellularis
 <400> 18

Met Tyr Asn Ile Ile Asn Lys His Gln Ile Ile Lys Ile Leu Leu Phe
 1 5 10 15
 Ser Leu Cys Val Phe Phe Phe Thr Leu Thr Glu Lys Gln Lys Ile Tyr
 20 25 30
 Ala Ala Asp Val Phe Phe Glu Gly Arg Thr Glu Thr Leu Ile Asn Val
 35 40 45
 Asn Lys Pro Phe Asp Ser Phe Phe Gly Gly Ser Asp Ser Thr Ile Gly
 50 55 60
 Thr Leu Glu Thr Gly Pro Thr Asn Leu Thr Phe Thr Thr Val Gly Ala

Substitute Sequence Listing

65		70		75		80
Phe	Arg	Asn	Ser	Val	Phe	Arg
			85		Ile	Ile
				Gly	Gly	Gly
				90		Arg
					Ser	Ser
					95	Phe
Asn	Asn	Pro	Asn	Thr	Val	Lys
			100		Gly	Asn
				105	Val	Thr
					Leu	Thr
					110	Tyr
					Asn	Arg
					115	Gly
					120	Leu
Thr	Asp	Val	Glu	Arg	Ile	Ile
		115			Gly	Ala
					120	Gly
					Ile	Ser
					125	Asn
						Arg
						Gly
						Leu
Val	Thr	Val	Thr	Gly	Ser	Val
	130				135	Asn
					Met	Lys
					Leu	Glu
					140	Asn
					Val	Ser
						Val
Thr	Arg	Gly	Ile	Tyr	Gly	Gly
					150	Val
					Tyr	Thr
					Gln	Asn
					155	Gly
						His
						Val
						Leu
Gly	Ser	Ile	Asn	Met	His	Leu
				165		Lys
					Asn	Val
					170	Gln
					Thr	Pro
						Leu
						Leu
						Ile
Gly	Ser	Gly	Val	Ser	Asn	Gly
			180			Pro
					Asn	Arg
					185	Ile
					Thr	Val
						Asn
						Gly
						Asp
Ile	Asn	Ile	Asp	Val	Glu	Asp
		195				Ser
						Arg
						Ile
						Gln
						Tyr
						Val
						Asn
						Ile
						Thr
Gly	Glu	Val	Asp	Ala	Gly	Ile
	210					Lys
						Gly
						Asn
						Ala
						Thr
						Leu
						Thr
						Val
						Lys
Lys	Ser	Thr	Val	Glu	Leu	Ile
					230	Asn
						Ser
						Gly
						Arg
						235
						Gly
						Asn
						Ile
						Leu
						Gly
						240
Asn	Leu	Lys	Ile	Ser	Ile	Ala
				245		Asp
					Ser	Asn
					250	Ile
						Arg
						Gly
						Leu
						Ser
						255
Val	Asp	Phe	Gly	Ser	Ser	Val
			260			Tyr
						Gly
						Asp
						Thr
						Ser
						Ile
						Asn
						Val
						Ile
Asn	Ser	Gln	Ile	Asn	Asp	Ile
		275				Thr
						Leu
						Ile
						Pro
						Arg
						Ala
						285
						Gly
						Gly
						Met
Leu	Val	Gly	Pro	Val	Thr	Leu
	290					Asp
						Ile
						Thr
						Ser
						300
						Thr
						Ile
						Gln
						Asn
Ile	Gln	Cys	Gly	Pro	Val	Ser
					310	Gln
						Asn
						Asn
						Gln
						315
						Leu
						Asn
						Thr
						Leu
						Asn
						320

Substitute Sequence Listing

Val Thr Val Asn Thr Ser Asn Ile Thr Asn Leu Asn Leu Gly Ser Val
325 330 335

Glu Gly His Thr Ile Ser Thr Thr Ala Thr Val Thr Asp Ser Asn Ile
340 345 350

Thr Asn Leu Asn Val Gly Thr Phe Asn Gly Leu Gly Val Thr Glu Asn
355 360 365

Ala Ser Val Ile Ile Asn Ser Gly Asn Ile Thr Asn Leu Asn Val Gly
370 375 380

Thr Asn Val Ile Ala Ala Ala Thr Thr Ile Asn Ser Ser Ala Thr Ile
385 390 395 400

His Asp Gly Leu Ile Ala Asn Leu Thr Leu Gly Ser Gln Gly Asn Gly
405 410 415

Arg Thr Met Ile Ala Thr Ala Asn Val Asn Gly Gly Thr Ile Gly Leu
420 425 430

Leu Thr Met Gly Ser Glu Asn Phe Ile Pro Gly Thr Arg Pro Ile Thr
435 440 445

Glu Leu Ala Ile Leu Asn Met Ser Gly Gly Leu Ile Glu Arg Ile Ile
450 455 460

Val Gly Asn Ala Asn Ser Ser Thr Ile Asn Phe Thr Pro Gly Lys Arg
465 470 475 480

Ser Ile Val Lys Thr Ile Asn Gly Pro Glu Leu Pro Tyr Leu Val Asn
485 490 495

Ile Gln Lys Gly Ala Met Thr Gln Trp Gly Thr Lys Asn Met Pro Phe
500 505 510

Leu Leu Asp Thr Arg Asn Leu Ile Leu Ser Gly Thr Leu Ile Thr Ser
515 520 525

Asn Ile Gln Leu Ala Asp Leu Ser Ile Thr Asn Leu Phe Val Ala Asn
530 535 540

Gly Gly Thr Leu Val Pro Arg Lys Leu Ile Pro Gly Asn Gln Pro Val
545 550 555 560

Ile Gln Phe Leu Gly Gly Pro Gln Ser Leu Leu Val Ile His Gln Pro
565 570 575

Substitute Sequence Listing

Leu Lys Val Asn Leu Ser Leu Ser Pro Lys Leu Ile Gly Ser Ser Met
580 585 590

Val Pro Leu Ala Phe Val Ser Gln Ser Phe Ser Ser Pro Asp Leu Phe
595 600 605

Val Lys Gln Thr Arg Ser Gly Leu Ile Trp Ser Asp Leu Glu Phe Asp
610 615 620

Pro Thr Thr Ser Ile Trp Tyr Val Asn Asn Ile Gln Ala Ser Gln Asp
625 630 635 640

Phe Tyr Ser Phe Ser Ile Ala Arg Glu Thr Thr Asn Trp Leu Arg Gln
645 650 655

Gln His Ile Trp Thr Leu Gln Asn Arg Ser Ser Lys Leu Leu Asp Asn
660 665 670

Glu His Tyr Gly Leu Trp Ile Asn Val Gln Gly Gly His Glu Ser Leu
675 680 685

Asp Thr Ser Ile Gly Ser Lys Ala Lys Met Pro Trp Ile Met Ala Thr
690 695 700

Ala Gly Tyr Asp Tyr Leu Gln Gln Leu Pro Arg Leu Asp Met Lys Ala
705 710 715 720

Leu Tyr Gly Leu Ala Phe Gly Ala Ser Lys Gly Lys Ser Lys Trp Ser
725 730 735

Ser Val Asn Ser Thr Lys Asn Asp Ala Glu Leu Gly Met Val Ser Gly
740 745 750

Tyr Val Gly Leu Ile His Asn Lys Thr Gly Leu Tyr Ser Thr Leu Thr
755 760 765

Leu Gln Leu Ala Ser Ser Lys Leu His Thr Asn Ser Thr Gly Phe Tyr
770 775 780

Arg Asn Phe Lys Trp Thr Glu Thr Thr Pro Thr Glu Ala Leu Glu Leu
785 790 795 800

Gly Trp Lys Tyr Thr Phe Asn Asn Gly Ile Lys Met Asn Pro Arg Gly
805 810 815

Gln Leu Ile Phe Glu Gln Thr Ser Lys His His Phe Asp Leu Gly Ile
820 825 830

Substitute Sequence Listing

Gln Asn Asp Lys Ala Ile Leu Asp Lys Ser Gln Leu Ile Thr Ser Ser
835 840 845

Leu Gly Ile Thr Val Glu Tyr Lys Leu Pro Val Thr Thr Pro Ile Asn
850 855 860

Leu Tyr Ala Gly Ile Glu Arg Ile Lys Gly Gln Ser Gly Asn Phe Ala
865 870 875 880

Ile Ser Ser Gln Ser Leu Gln Met Lys Phe Lys His Asp Asn Asp Thr
885 890 895

Ser Val Val Arg Ala Thr Ile Gly Thr Asn Ile Leu Leu Gly Glu His
900 905 910

Phe Asn Ile His Cys Asp Ile Phe Gly Asp Lys Gly Asn Asp Lys Gly
915 920 925

Ile Gly Gly Gln Ala Gly Phe Thr Tyr Lys Phe
930 935